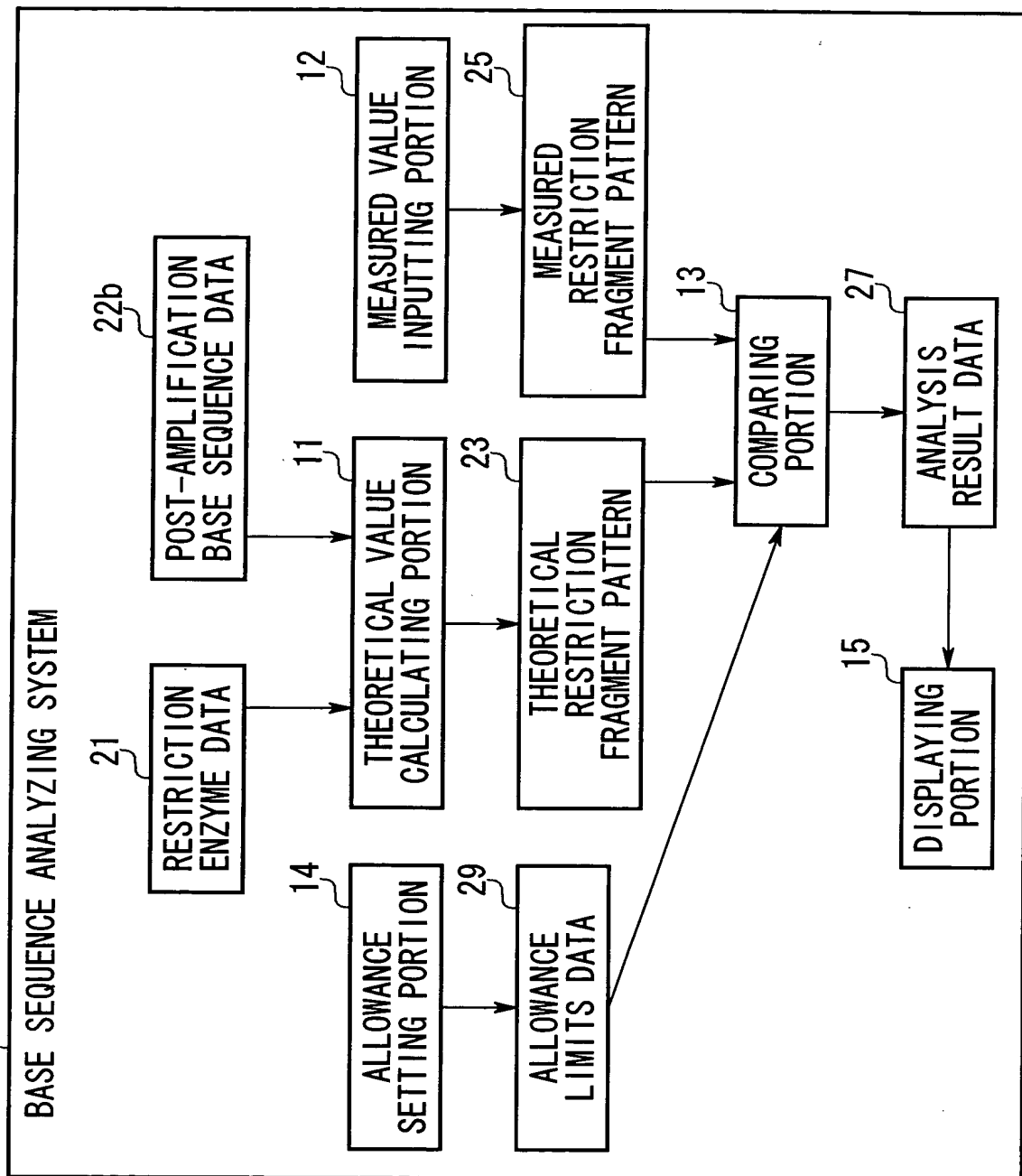


FIG. 1



APPROVED	U.G. FIG.	
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FIG. 2

LOCUS RSP16SRRZ 1490 bp rRNA BCT 04-DEC-1995
DEFINITION Rhodospirillum salexigens 16S ribosomal RNA.
ACCESSION M59070
NID g175871
VERSION M59070.1 GI:175871
KEYWORDS 16S ribosomal RNA.
SOURCE Rhodospirillum salexigens rRNA.
ORGANISM Rhodothalassium salexigens
Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Rhodothalassium.
REFERENCE 1 (bases 1 to 1490)
AUTHORS Woese, C. R.
TITLE A phylogenetic analysis of the some purple bacteria
JOURNAL Unpublished (1991)
FEATURES Location/Qualifiers
source 1..1490
/organism="Rhodothalassium salexigens"
/db_xref="taxon:1086"
/tissue_lib="DSM 2132"
rRNA 1..1490
/gene="16S rRNA"
/product="16S ribosomal RNA"
gene 1..1490
/gene="16S rRNA"
BASE COUNT 342 a 343 c 472 g 284 t 49 others

090075.0100

APPROVED	O.G. FIG.	
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FIG. 3

ORIGIN

1 gctcagaacg aacgctggcg gcaggcctaa cacatgcaag tcgagcgcan nccttcgggg
61 gtnagcggcg gacgggtgag taacgcgtgg gaacctgctc agggctctgg gataactgct
121 ggaaacggca gctaataccg gatacgccgt attgggaaag aaattcggcc ttggatgggc
181 ccgcgttggg ttagctagat ggtggggtaa cggcctacca tggcgacgat ccatagctgg
241 tttgagagga tgatcagcca cactgggact gagacacggc ccagactcct acgggaggga
301 gcagtgggga atcttagaca atgggggcaa ccctgatcta gccatgccgc gtgagtgatg
361 aaggccttag ggttgtaaag ctctttcagc agggaagata atgactgtac ctgcagaaga
421 agctccggct aactccgtgc cagcagccgc ggtaatacgg agngggcnag cgttggtcgg
481 aattactggg cgtaaagcgc gcgtaggcgg atcggtcagt tgggggtgaa agcccggggc
541 tcaacctcgg aactgccctc aaaactaccg atcnagagtt cgggagaggt aagcggaatt
601 ccagtgtag aggtgaaatt cgtagatatt gggaagaaca ccagtggcga aggocggctta
661 ctggaccgat actgacgctg aggtgcnaaa gcgtggggag caaacaggat tagataccct
721 ggtagtccac gccgtaaacg atgggtgcta gatgtcgggg ctcttagagt ttcggtatcg
781 cagctaacgc attaagcacc ccgccngggg agtacggccg caagggtaaa actcaaagga
841 attgacgggg gcnngcacaa gcggtggagc atgtggttta attcgaanna acgcgcagaa
901 ccttaccagc tcttgacatc ccgggacgac ttccagagat ggattttttc acttcggtga
961 cccgngaca ggtgctgcat ggctgtcgtc agctcgtgtc gtgagatgt

//

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIG. 4

RESTRICTION ENZYME DATA

RESTRICTION ENZYME NUMBER	RESTRICTION ENZYME NAME	RECOGNITION SITE	RESTRICTION SITE
1	AluI	agct	2
2	HaeIII	ggcc	2
3	RsaI	gtac	2
4	ScrFI	ccngg	2
5	HhaI	gcgc	2
6	BamHI	ggatcc	1
7	EcoRI	gaatt	1
8	HindIII	aagctt	1
9	PstI	ctgcag	5
10	PvuII	cagctg	3
11	SaII	gagctc	5
12	SmaI	cccggg	3
13	XbaI	tctaga	1

0900876-071001

FIG. 5

FIG. 5

TKS030

✕

DATABASE RECORD (THEORETICAL VALUES)

BASE SEQUENCE FILE
 AB021410.TXT
 AF064459.TXT
 AJ002302.TXT
 L01165.TXT
 U96927.TXT
 X95918.TXT
 Y10657.TXT
 Z69293.TXT

→

RESTRICTION ENZYME
 Acl
 Hael
 Haa
 Rsa
 abd

RESTRICTION FRAGMENT
 LENGTH CALCULATION

RETURN

FIG. 6

FIG. 6

THEORETICAL RESTRICTION FRAGMENT PATTERNS

DNA NUMBER	NUMERICAL VALUE SECTION	GROUP NAME	NAME OF ORGANISM	NAME OF GENE	RESTRICTION ENZYME NUMBER	RESTRICTION FRAGMENT LENGTH VALUE
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	2	204
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	5	509
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	5	542
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	3	194
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	3	457
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	3	400
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	2	156
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	2	90
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	2	317
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	2	169
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	1	550
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	1	180
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	1	79
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	1	87
AB000278	1		Vibrio iliopiscarius	16S rRNA; 16S ribosomal RNA	2	105
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	156
AB038030	1		Vibrio splendidus	16S ribosomal RNA	5	509
AB038030	1		Vibrio splendidus	16S ribosomal RNA	5	565
AB038030	1		Vibrio splendidus	16S ribosomal RNA	4	1074
AB038030	1		Vibrio splendidus	16S ribosomal RNA	3	194
AB038030	1		Vibrio splendidus	16S ribosomal RNA	3	234
AB038030	1		Vibrio splendidus	16S ribosomal RNA	3	223
AB038030	1		Vibrio splendidus	16S ribosomal RNA	3	423
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	90
AB038030	1		Vibrio splendidus	16S ribosomal RNA	1	175
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	204
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	317
AB038030	1		Vibrio splendidus	16S ribosomal RNA	2	105
AB038030	1		Vibrio splendidus	16S ribosomal RNA	1	236
AB038030	1		Vibrio splendidus	16S ribosomal RNA	1	572

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FIG. 7

TKS040

MOLECULAR WEIGHT FILE

Deni01(Ha).txt
DNA.xls

GROUP NAME

AP

DNA NUMBER

AP1

RESTRICTION ENZYME

AluI

RESTRICTION FRAGMENT LENGTH

100	200	300							

ENTER

RETURN

DATABASE RECORDING (MEASURED VALUE)

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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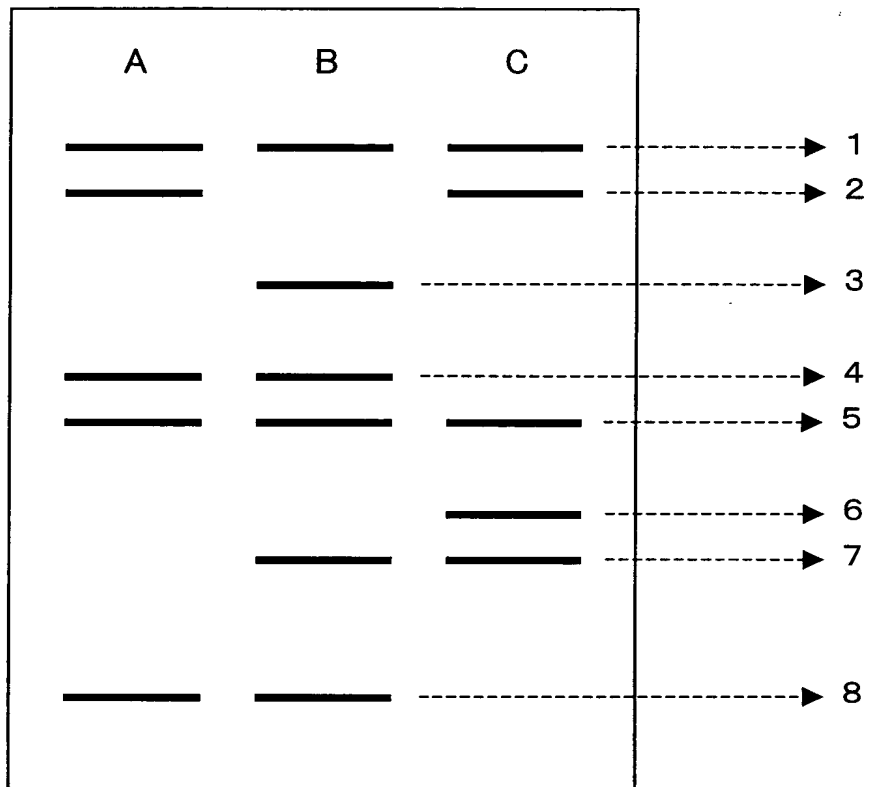
FOOT 20" 92800650

FIG. 8

MEASURED RESTRICTION FRAGMENT PATTERNS

DNA NUMBER	NUMERICAL VALUE SECTION	GROUP NAME	NAME OF ORGANISM	NAME OF GENE	RESTRICTION ENZYME NUMBER	MEASURED RESTRICTION FRAGMENT LENGTH VALUE
AP1	2	AP			1	100
AP1	2	AP			1	200
AP1	2	AP			1	300

FIG. 9



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FIG. 10A

	A	B	C	D
A	—	—	—	—
B	0.7	—	—	—
C	0.8	0.5	—	—
D	0.1	0.4	0.3	—

FIG. 10A

*1

$$S(B, A + C) = \frac{S(B, A) + S(B, C)}{2}$$

*2

$$S(D, A + C) = \frac{S(D, A) + S(D, C)}{2}$$

	A+C	B	D
A+C	—	—	—
B	0.6 (*1)	—	—
D	0.2 (*2)	0.4	—

FIG. 10B

*3

$$S(D, (A + C) + B) = \frac{S(D, A + C) + S(D, B)}{2}$$

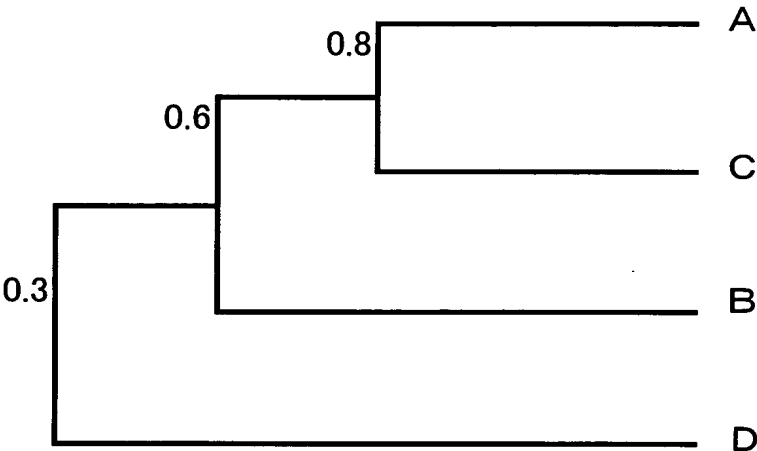
	(A+C)+B	D
(A+C)+B	—	—
D	0.3 (*3)	—

FIG. 10C

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
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FIG. 11



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FIG. 12

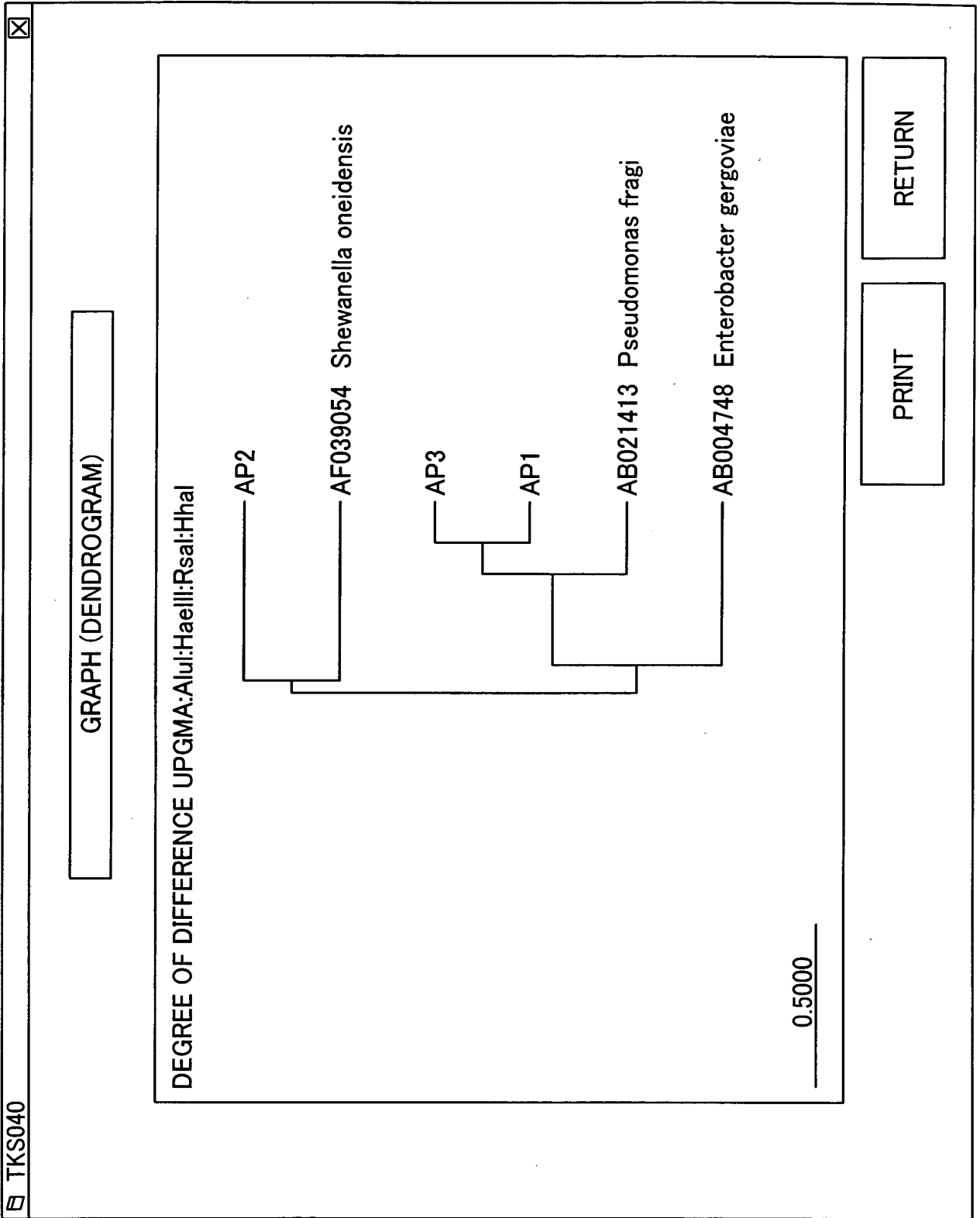


FIG. 13

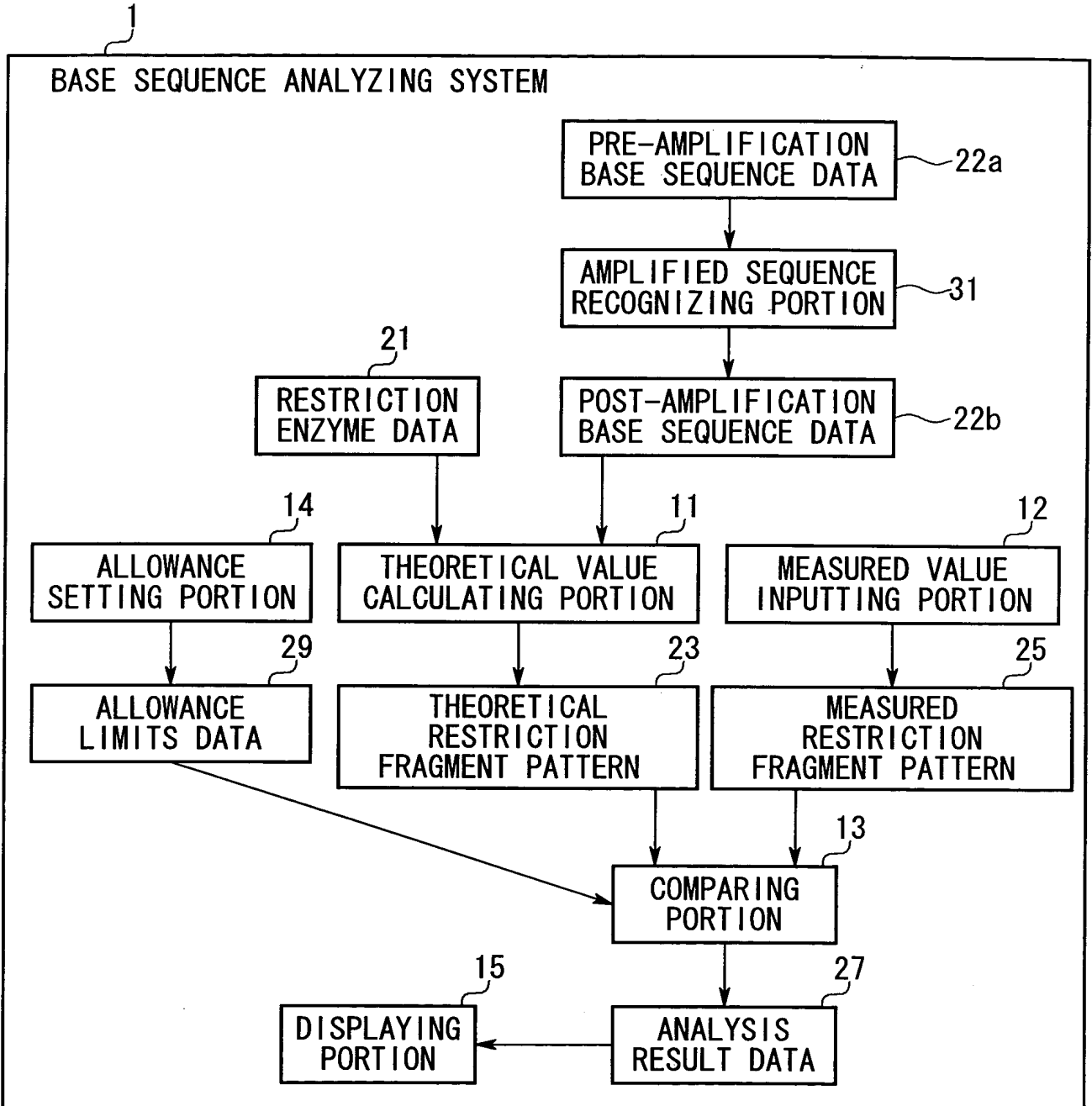


FIG. 13

APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIG. 14

LOCUS RSP16SRRZ 1490 bp rRNA BCT 04-DEC-1995
DEFINITION Rhodospirillum salexigens 16S ribosomal RNA.
ACCESSION M59070
NID g175871
VERSION M59070.1 GI:175871
KEYWORDS 16S ribosomal RNA.
SOURCE Rhodospirillum salexigens rRNA.
ORGANISM Rhodothalassium salexigens
Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae;
Rhodothalassium.
REFERENCE 1 (bases 1 to 1490)
AUTHORS Woese, C. R.
TITLE A phylogenetic analysis of the some purple bacteria
JOURNAL Unpublished (1991)
FEATURES Location/Qualifiers
source 1..1490
/organism="Rhodothalassium salexigens"
/db_xref="taxon:1086"
/tissue_lib="DSM 2132"
rRNA 1..1490
/gene="16S rRNA"
/product="16S ribosomal RNA"
gene 1..1490
/gene="16S rRNA"
BASE COUNT 342 a 343 c 472 g 284 t 49 others

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APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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FIG. 15

ORIGIN

1 ncaacatgag agtttgatcc tggctcagaa cgaacgctgg cggcaggcct aacacatgca
61 agtcgagcgc annccctcgg gggtnagcgg cggacgggtg agtaacgcgt gggaacctgc
121 tcagggctct gggataactg ctggaaacgg cagctaatac cggatacgcc gtattgggaa
181 agaaattcgg ccttggatgg gcccgcttg gattagctag atggtggggt aacggcctac
241 catggcgacg atccatagct ggtttgagag gatgatcagc cacactggga ctgagacacg
301 gccagactc ctacgggagg cagcagtggg gaatcttaga caatgggggc aacctgatc
361 tagccatgcc gcgtgagtga tgaaggcctt agggttgtaa agctcttica gcagggaaga
421 taatgactgt acctgcagaa gaagctccgg ctaactccgt gccagcagcc gcggtaatac
481 ggagngggcn agcgttggtc ggaattactg ggcgtaaagc gcgcgtaggc ggatcggtca
541 gttgggggtg aaagcccggg gctcaacctc ggaactgccc taaaactac cgatcnagag
601 ttcgggagag gtaagcggaa ttcccagtgt agaggtgaaa ttcgtagata ttgggaagaa
661 caccagtggc gaaggcggct tactggaccg atactgacgc tgaggtgcn aagcgtgggg
721 agcaaacagg attagatacc ctggtagtcc acgccgtaaa cgatgggtgc tagatgtcgg
781 ggctcttaga gtttcggtat cgcagctaac gcattaagca ccccgcnngg ggagtacggc
841 cgcaaggtta aaactcaaag gaattgacgg gggcnngcac aagcggtgga gcatgtggtt
901 taattcgaan naacgcgcag aaccttacc gctcttgaca tccggggacg acttccagag
961 atggattttt tcacttcggt gacccgnga caggtgctgc atggctgtcg tcagctcgtg
1021 tcgtgagatg ttgggttaag tccncaacg agcgcaaccc tcgcccttag ttgccagcat
1081 ttggttgggg actctaaggg aactgccggt gataagccgg aggaagggtg ggatgacgtc
1141 aagtcctcat ggcccttatg ggctgggcta cacacgtgct acaatggcgg tgacagaggg
1201 cagcgagcct gcgagggtga gcgaatctct aaaagccgtc tcagttcgga ttgttctctg
1261 caactcgaga gcatgaagg ggaatcgcta gtaatcgcg atcagcatgc cgcggtgaat
1321 acgttcccgg gnnttgatca caccgccgt cacaccatgg gagttggtt gaccgaaga
1381 cggtagacta acccgaaagg ggggcagncg gccacggtca ggtcagcgac tggggtnnnn
1441 nngtaacaag nnnnnnnnnn nnnnnnnnnn nnnngatca cctcctttct

//

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FIG. 16

SEQUENCE OF FORWARD PRIMER, NAME (ALPHABET OR FIGURE: 5 OR LESS)

5' gctcagattgaactcggcg; 41f

ALLOWANCE LIMITS FOR MISMATCH 4

SEQUENCE OF REVERSE PRIMER, NAME (ALPHABET OR FIGURE: 5 OR LESS)

5' acatttcacacacagctg; 1066r

ALLOWANCE LIMITS FOR MISMATCH 4

41f-1066r

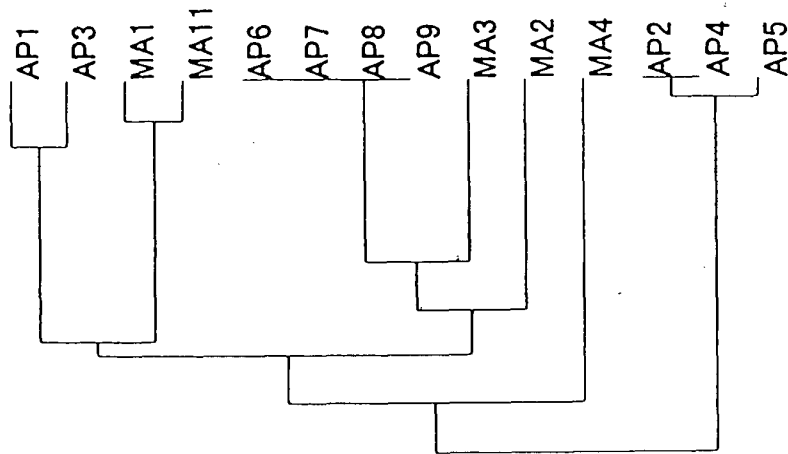
AF00128
AF00225
X00881

AB00120
AF00232
AF01122
D01255
D01388
D10115
D12303
X12450
X13450
X13451
X80885

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FIG. 17

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:RsaI:HhaI



0.5000

FIG. 18

FIG. 18

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:Rsal:HhaI



FIG. 19

FIG. 19

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:Rsal:HhaI

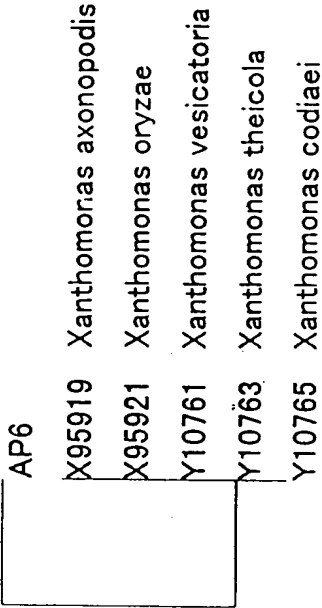
AP3	
D84004	Flavimonas oryzihabitans
D84015	Pseudomonas fulva
D84020	Pseudomonas putida
D84023	Pseudomonas straminea
Z76653	Pseudomonas alcaligenes

0.5000

FOOT 20 " 92800650

FIG. 20

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:Rsal:HhaI



0.5000

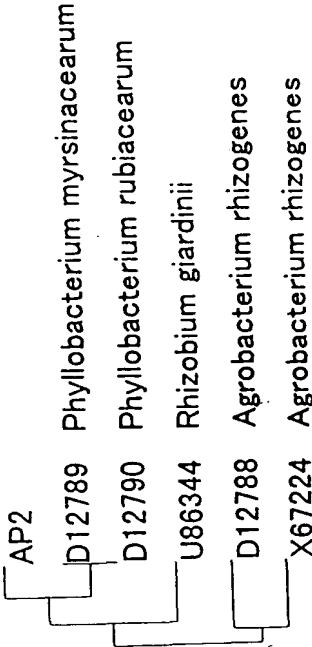
BY DRAFTSMAN	U.S. P.T.O.	
	CLASS	SUBCLASS

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FIG. 21

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI



0.5000

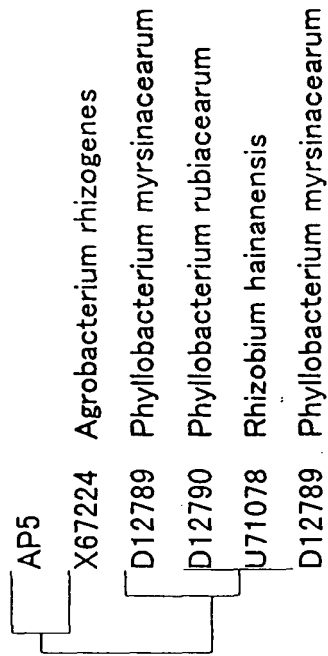
BY	CLASS	SUBCLASS
DRAFTSMAN		

OBLÓN, SPIVÁK, ET AL
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INV: Katsuji WATANABE, et al.
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FIG. 22

DEGREE OF DIFFERENCE UPGMA:Alul:HaeIII:RsaI:HhaI

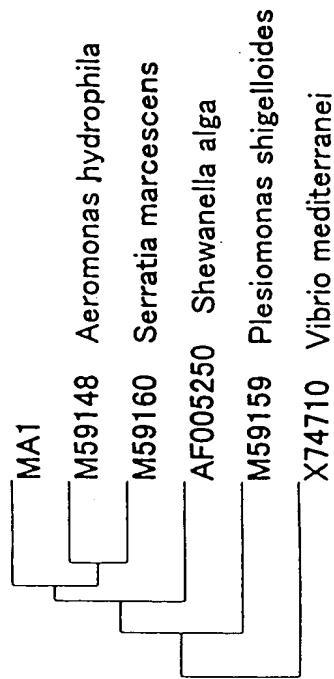


0.5000

FIG. 23

FIG. 23

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI



0.5000

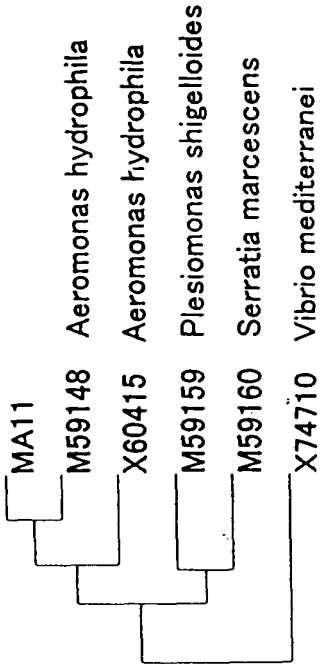
APPROVED	O.G. FIG.	
BY	CLASS	SUBCLASS
DRAFTSMAN		

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INV: Katsuji WATANABE, et al.
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FIG. 24

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI

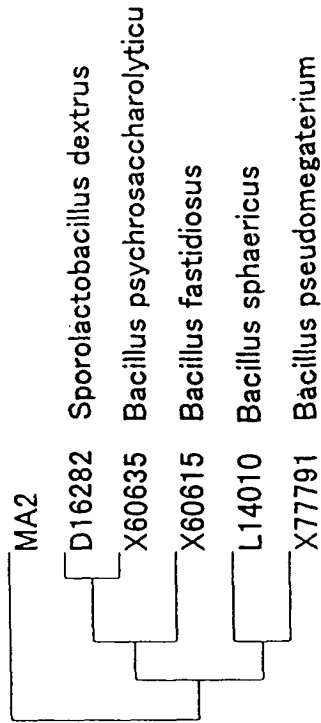


0.5000

FIG. 25

FIG. 25

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI

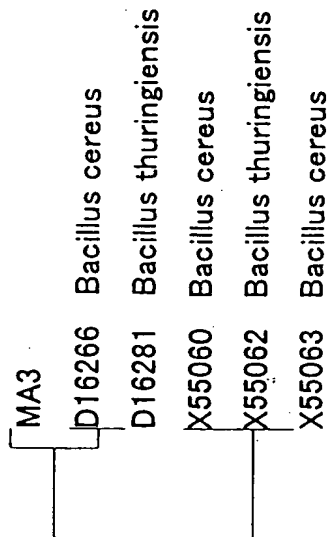


0.5000

FIG. 26

FIG. 26

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI



0.5000

FOOT 20" 92800650

FIG. 27

DEGREE OF DIFFERENCE UPGMA:AluI:HaeIII:RsaI:HhaI



0.5000

FIG. 28

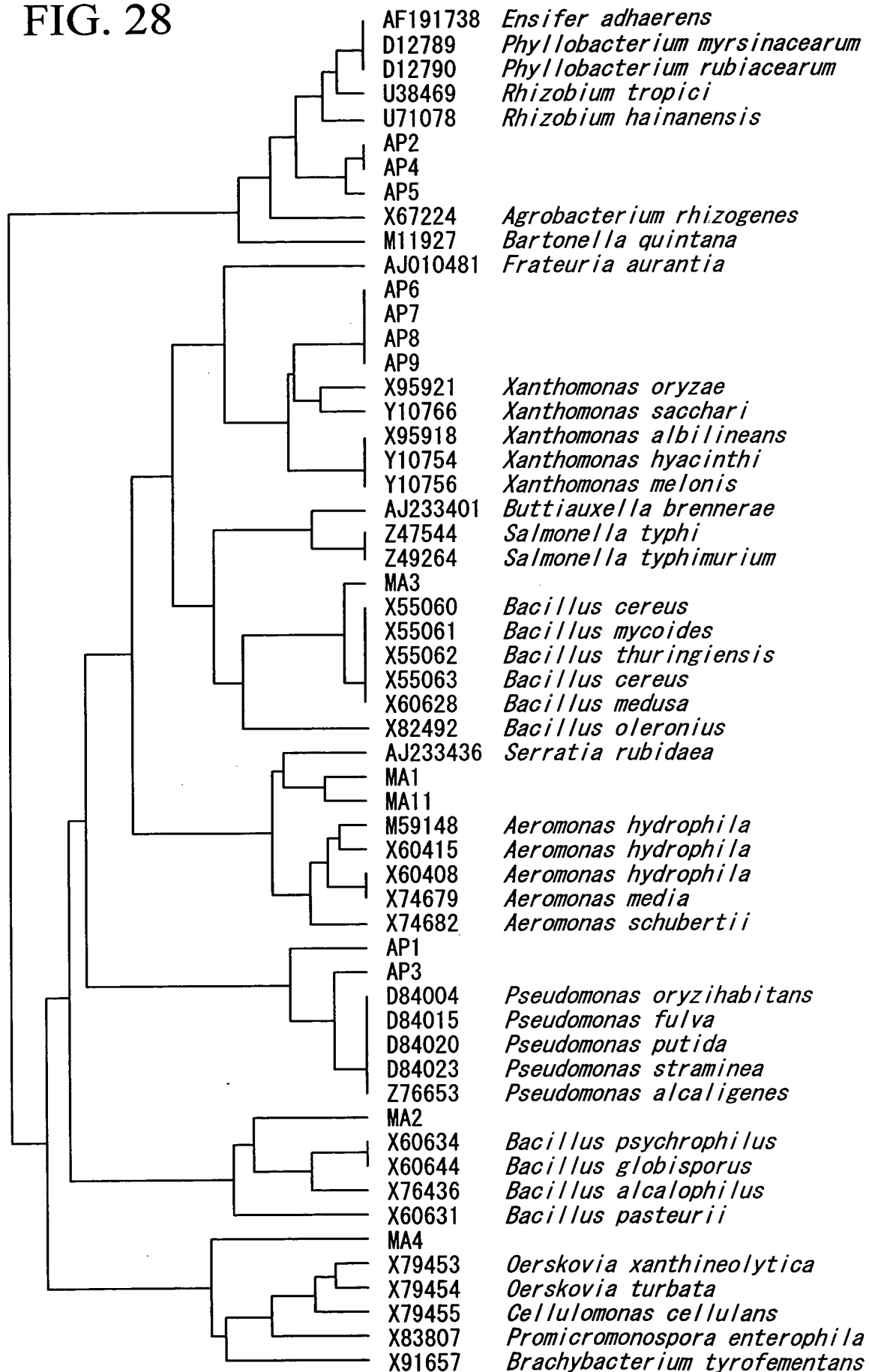


FIG. 28

FOOTNOTES

FIG. 29

CLASSIFICATION OF ISOLATED DENITRIFYING BACTERIA by 16S rDNA RFLP (RESTRICTION ENZYME HaeIII, HhaI, AluI, RsaI, SrfI) AND COMPARISON OF IDENTIFICATION RESULTS BY HOMOLOGY SEARCH OF BASE SEQUENCES

GROUP	R OF BACRFLP	BASE SEQUENCE (% HOMOLOGY)
I	20	<i>Enterobacteriaceae</i>
II	9	<i>Burkholderia</i> genus.
III+IV	12	<i>Ralstonia</i> genus
V	6	<i>Comamonas acidovorans</i>
VI+VIII	32	<i>Pseudomonas</i> genus
VII	20	<i>P. putida</i>
IX	8	<i>P. rhodesiae</i>
X	5	<i>P. stutzeri</i>
XI	3	<i>Acinetobacter haemolyticus</i>
XII	18	<i>Pseudomonas</i> genus
XIII	1	<i>Acivorax delafieldii</i>

	<i>Klebsiella</i> genus (100%)
	<i>B. vietnamiensis</i> (96.9%, 92.6%, 93.0%, 94.8%, 93.4%), <i>Burkholderia</i> genus (100%)
	<i>Ralstonia</i> genus (92.0%, 94.5%, 94.5%), <i>R. paucula</i> (95.1%, 93.8%), <i>R. eutropha</i> (95.6%, 100%, 96.7%)
	<i>C. acidovorans</i> (98.2%, 100%)
	<i>P. putida</i> (97.7%, 99.0%, 99.2%), <i>P. fluorescens</i> (95.8%, 99.5%), <i>P. rhodesiae</i> (98.4%)
	<i>P. putida</i> (100%)
	<i>P. rhodesiae</i> (98.5%, 99.5%)
	<i>P. stutzeri</i> (98.0%, 94.6%, 92.0%)
	<i>A. haemolyticus</i> (96.1%)
	<i>Pseudomonas</i> genus (99.5%)
	<i>Acivorax delafieldii</i> (94.7%)